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## **Table of content**

Figure S1. Catalytic site of VIM-1S	32
Figure S2. Comparison of VIM-1 and IMP-1 binding siteS	3
Figure S3. Crystallographic orientation of a 1,2,4-triazole-3-thiol compound in L1 MBLS	\$4
Table S1. Enzymatic inhibitor activity of compounds 1a-g and 2a-g against VIM-1, IMP-1 and KPC   2	C- 55
<b>Table S2.</b> MICs of meropenem in combination with compounds 1a-g and 2a-g	36
<sup>1</sup> H and <sup>13</sup> C NMR spectra of compounds 1a-g and 2a-gS	57

**Figure S1.** Catalytic site in VIM-1 apo form (PDB code 5n5g). Protein structure is reported in cartoon representation, zinc atoms are shown as grey spheres, bridging water Wat1 and coordinating water Wat2 have been depicted as red spheres and labelled, significant residues coordinating the zinc atoms or lining the binding pocket are shown as sticks, coordination bonds are reported as dashed lines. Loops L3 (red) and L10 (green) are highlighted.



Figure S2. Comparison of VIM-1 (a) and IMP-1 (b) binding site. Protein structure is reported in cartoon representation, zinc atoms are shown as grey spheres, significant residues coordinating the zinc atoms or lining the binding pocket are shown as sticks, coordination bonds are reported as dashed lines.





**Figure S3.** Crystallographic orientation of a 1,2,4-triazole-3-thiol compound in L1 MBL (PDB CODE 5dpx). Protein structure is reported in cartoon representation, zinc atoms are shown as grey spheres, significant residues coordinating the zinc atoms or lining the binding pocket are shown as sticks, coordination bonds are reported as dashed lines.



Code	VIM-1 K <sub>i</sub> (µM)	IMP-1 % of inhibition at 200 μΜ	KPC-2 % of inhibition at 200 μM
1a	601	37	20
1b	137	51	17
1c	182	44	6
1e	204	44	15
1g	n.t.	n.t	n.t
2a	50,3	46	18
2c	124	45	4
2d	66,9	45	33
<b>2e</b>	142	46	7
<b>2f</b>	145	40	21

Table S1. Enzymatic Inhibitor Activity	of	compounds	1a-g	and	2a-g	against	VIM-1,	IMP-1	and
KPC-2 not included in Table 1.									

Table S2. MICs of meropenem in combination with compounds 1a-g and 2a-g

Clinical strains of *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *P. aeruginosa* producing NDM-1, VIM-2, IMP-28 and KPC-2 were used. The MIC was calculated through the microdilution method using 96-microwell plates. The bacterial inoculum in each well was adjusted at a final dilution of 1:1000 from an overnight culture. Meropenem (MEM) was mixed with every compound maintaining a mole ratio of 1:1 in all the wells.

$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	ml)
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MEM + 1c 512 MEM + 1d 64   MEM + 1d 512 MEM + 1e 64   MEM + 1e 512 MEM + 1g 64	
MEM + 1d   512   MEM + 1e   64     MEM + 1e   512   MEM + 1g   64	
MEM + 1e 512 MEM + 1g 64	
MEM + 1g 512 MEM + 2b 64	
MEM + 2b 512 MEM + 2c 64	
MEM + 2c 256 MEM + 2e 64	
MEM + 2e $256 - 512$ MEM + 2f 64	
MEM + 2g 512 MEM + 2g 64	

P. aeruginosa VIM-2	MIC (µg/ml)
Meropenem (MEM)	8
MEM + 2f	8
MEM + 1a	8
MEM + 1b	8
MEM + 1c	8
MEM + 1d	8
MEM + 1e	8
MEM + 1g	8
MEM + 2b	8
MEM + 2c	8
MEM + 2e	8
MEM + 2g	8

K. pneumoniae 53A9 KPC-2	MIC (µg/ml)
Meropenem (MEM)	64
MEM + 1a	64
MEM + 1b	64
MEM + 1c	64
MEM + 1d	64
MEM + 1e	64
MEM + 1g	64
MEM + 2b	64
MEM + 2c	64
MEM + 2e	64
MEM + 2f	64
MEM + 2g	32

P. aeruginosa IMP-28	MIC (µg/ml)
Meropenem (MEM)	16
MEM + 2f	16
MEM + 1a	16
MEM + 1b	16
MEM + 1c	16
MEM + 1d	16
MEM + 1e	16
MEM + 1g	16
MEM + 2b	16
MEM + 2c	16
MEM + 2e	16
MEM + 2g	16

## <sup>1</sup>H and <sup>13</sup>C NMR spectra of compounds 1a-g and 2a-g





1b



1c



1d



**1e** 



1f



1g









**2b** 







2d





**2e** 







2g

